

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/524,765  
Source: PT/10  
Date Processed by STIC: 2/28/05

# ***ENTERED***



PCT

## RAW SEQUENCE LISTING

DATE: 02/28/2005

PATENT APPLICATION: US/10/524,765

TIME: 10:16:57

Input Set : A:\532622010700seq.txt

Output Set: N:\CRF4\02282005\J524765.raw

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3 <110> APPLICANT: Plesch, Gunnar
4      Blau, Astrid
5      Daschner, Klaus
7 <120> TITLE OF INVENTION: Method for Identifying Herbicidally Active Substances
9 <130> FILE REFERENCE: 532622010700
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/524,765
C--> 12 <141> CURRENT FILING DATE: 2005-02-16
14 <150> PRIOR APPLICATION NUMBER: PCT/EP03/08393
15 <151> PRIOR FILING DATE: 2003-07-30
17 <160> NUMBER OF SEQ ID NOS: 52
19 <170> SOFTWARE: PatentIn version 3.1
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 1230
23 <212> TYPE: DNA
24 <213> ORGANISM: Arabidopsis thaliana
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (1)..(1230)
29 <223> OTHER INFORMATION:
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34 Met Ala Ala Lys Ile Ile Gly Gly Cys Cys Ser Trp Arg Arg Phe Tyr
35 1          5          10          15
37 agg aag aga aca tca tct cga ttt ctg att ttc tct gtt cga gcc tct      96
38 Arg Lys Arg Thr Ser Ser Arg Phe Leu Ile Phe Ser Val Arg Ala Ser
39          20          25          30
41 agt tcc atg gat gac atg gac acc gtc tac aag caa ttg gga ttg ttt      144
42 Ser Ser Met Asp Asp Met Asp Thr Val Tyr Lys Gln Leu Gly Leu Phe
43          35          40          45
45 tca cta aag aag aag att aaa gat gtt gtt ctt aag gct gag atg ttt      192
46 Ser Leu Lys Lys Lys Ile Lys Asp Val Val Leu Lys Ala Glu Met Phe
47          50          55          60
49 gca ccg gat gct ctt gag ctt gaa gaa gag cag tgg ata aag caa gaa      240
50 Ala Pro Asp Ala Leu Glu Leu Glu Glu Glu Gln Trp Ile Lys Gln Glu
51 65          70          75          80
53 gaa aca atg cgt tac ttt gat tta tgg gat gat ccc gct aaa tct gat      288
54 Glu Thr Met Arg Tyr Phe Asp Leu Trp Asp Asp Pro Ala Lys Ser Asp
55          85          90          95
57 gag att ctt ctc aaa tta gct gat cga gct aaa gca gtc gat tcc ctc      336
58 Glu Ile Leu Leu Lys Leu Ala Asp Arg Ala Lys Ala Val Asp Ser Leu
59          100         105         110
61 aaa gac ctc aaa tac aag gct gaa gaa gct aag ctg atc ata caa ttg      384
62 Lys Asp Leu Lys Tyr Lys Ala Glu Glu Ala Lys Leu Ile Ile Gln Leu

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63	115	120	125	
65	ggt gag atg gat gct ata gat tac agt ctc ttt gag caa gcc tat gat	432		
66	Gly Glu Met Asp Ala Ile Asp Tyr Ser Leu Phe Glu Gln Ala Tyr Asp			
67	130	135	140	
69	tca tca ctc gat gta agt aga tcg ttg cat cac tat gag atg tct aag	480		
70	Ser Ser Leu Asp Val Ser Arg Ser Leu His His Tyr Glu Met Ser Lys			
71	145	150	155	160
73	ctt ctt agg gat caa tat gac gct gaa ggc gct tgt atg att atc aaa	528		
74	Leu Leu Arg Asp Gln Tyr Asp Ala Glu Gly Ala Cys Met Ile Ile Lys			
75	165	170	175	
77	tct gga tct cca ggc gca aaa tct cag gat ttg cag ata tgg aca gag	576		
78	Ser Gly Ser Pro Gly Ala Lys Ser Gln Asp Leu Gln Ile Trp Thr Glu			
79	180	185	190	
81	caa gtt gta agt atg tat atc aaa tgg gca gaa agg cta ggc caa aac	624		
82	Gln Val Val Ser Met Tyr Ile Lys Trp Ala Glu Arg Leu Gly Gln Asn			
83	195	200	205	
85	gcg cgg gtg gct gag aaa tgt agt tta ttg agt aat aaa agt ggc gta	672		
86	Ala Arg Val Ala Glu Lys Cys Ser Leu Leu Ser Asn Lys Ser Gly Val			
87	210	215	220	
89	agt tca gcc acg ata gag ttt gaa ttc gag ttt gct tat ggt tat ctc	720		
90	Ser Ser Ala Thr Ile Glu Phe Glu Phe Glu Phe Ala Tyr Gly Tyr Leu			
91	225	230	235	240
93	tta ggt gag cga ggt gtg cac cgc ctt atc ata agt tcc act tct aat	768		
94	Leu Gly Glu Arg Gly Val His Arg Leu Ile Ile Ser Ser Thr Ser Asn			
95	245	250	255	
97	gag gaa tgt tca gcg act gtt gat atc ata cca cta ttc ttg aga gca	816		
98	Glu Glu Cys Ser Ala Thr Val Asp Ile Ile Pro Leu Phe Leu Arg Ala			
99	260	265	270	
101	tct cct gat ttt gaa gta aag gaa ggt gat ttg att gta tcg tat cct	864		
102	Ser Pro Asp Phe Glu Val Lys Glu Gly Asp Leu Ile Val Ser Tyr Pro			
103	275	280	285	
105	gca aaa gag gat cac aaa ata gct gag aat atg gtt tgt atc cac cat	912		
106	Ala Lys Glu Asp His Lys Ile Ala Glu Asn Met Val Cys Ile His His			
107	290	295	300	
109	att ccg agt gga gta aca cta caa tct tca gga gaa aga aac cgg ttt	960		
110	Ile Pro Ser Gly Val Thr Leu Gln Ser Ser Gly Glu Arg Asn Arg Phe			
111	305	310	315	320
113	gca aac agg atc aaa gct cta aac cgg ttg aag gcg aag cta ctt gtg	1008		
114	Ala Asn Arg Ile Lys Ala Leu Asn Arg Leu Lys Ala Lys Leu Leu Val			
115	325	330	335	
117	ata gca aaa gag caa aag gtt tcg gat gta aat aaa atc gac agc aag	1056		
118	Ile Ala Lys Glu Gln Lys Val Ser Asp Val Asn Lys Ile Asp Ser Lys			
119	340	345	350	
121	aac att ttg gaa ccg cgg gaa gaa acc agg agt tat gtc tct aag ggt	1104		
122	Asn Ile Leu Glu Pro Arg Glu Glu Thr Arg Ser Tyr Val Ser Lys Gly			
123	355	360	365	
125	cac aag atg gtg gtt gat aga aaa acc ggt tta gag att ctg gac ctg	1152		
126	His Lys Met Val Val Asp Arg Lys Thr Gly Leu Glu Ile Leu Asp Leu			
127	370	375	380	

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129 aaa tcg gtc ttg gat gga aac att gga cca ctc ctt gga gct cat att      1200
130 Lys Ser Val Leu Asp Gly Asn Ile Gly Pro Leu Leu Gly Ala His Ile
131 385                      390                      395                      400
133 agc atg aga aga tca att gat gcg att tag                                1230
134 Ser Met Arg Arg Ser Ile Asp Ala Ile
135                      405
138 <210> SEQ ID NO: 2
139 <211> LENGTH: 409
140 <212> TYPE: PRT
141 <213> ORGANISM: Arabidopsis thaliana
143 <400> SEQUENCE: 2
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146 1                      5                      10                      15
149 Arg Lys Arg Thr Ser Ser Arg Phe Leu Ile Phe Ser Val Arg Ala Ser
150                      20                      25                      30
153 Ser Ser Met Asp Asp Met Asp Thr Val Tyr Lys Gln Leu Gly Leu Phe
154                      35                      40                      45
157 Ser Leu Lys Lys Lys Ile Lys Asp Val Val Leu Lys Ala Glu Met Phe
158                      50                      55                      60
161 Ala Pro Asp Ala Leu Glu Leu Glu Glu Glu Gln Trp Ile Lys Gln Glu
162 65                      70                      75                      80
165 Glu Thr Met Arg Tyr Phe Asp Leu Trp Asp Asp Pro Ala Lys Ser Asp
166                      85                      90                      95
169 Glu Ile Leu Leu Lys Leu Ala Asp Arg Ala Lys Ala Val Asp Ser Leu
170                      100                     105                     110
173 Lys Asp Leu Lys Tyr Lys Ala Glu Ala Lys Leu Ile Ile Gln Leu
174                      115                     120                     125
177 Gly Glu Met Asp Ala Ile Asp Tyr Ser Leu Phe Glu Gln Ala Tyr Asp
178                      130                     135                     140
181 Ser Ser Leu Asp Val Ser Arg Ser Leu His His Tyr Glu Met Ser Lys
182 145                      150                      155                      160
185 Leu Leu Arg Asp Gln Tyr Asp Ala Glu Gly Ala Cys Met Ile Ile Lys
186                      165                      170                      175
189 Ser Gly Ser Pro Gly Ala Lys Ser Gln Asp Leu Gln Ile Trp Thr Glu
190                      180                      185                      190
193 Gln Val Val Ser Met Tyr Ile Lys Trp Ala Glu Arg Leu Gly Gln Asn
194                      195                      200                      205
197 Ala Arg Val Ala Glu Lys Cys Ser Leu Leu Ser Asn Lys Ser Gly Val
198                      210                      215                      220
201 Ser Ser Ala Thr Ile Glu Phe Glu Phe Glu Phe Ala Tyr Gly Tyr Leu
202 225                      230                      235                      240
205 Leu Gly Glu Arg Gly Val His Arg Leu Ile Ile Ser Ser Thr Ser Asn
206                      245                      250                      255
209 Glu Glu Cys Ser Ala Thr Val Asp Ile Ile Pro Leu Phe Leu Arg Ala
210                      260                      265                      270
213 Ser Pro Asp Phe Glu Val Lys Glu Gly Asp Leu Ile Val Ser Tyr Pro
214                      275                      280                      285
217 Ala Lys Glu Asp His Lys Ile Ala Glu Asn Met Val Cys Ile His His
218                      290                      295                      300

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Input Set : A:\532622010700seq.txt

Output Set: N:\CRF4\02282005\J524765.raw

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221 Ile Pro Ser Gly Val Thr Leu Gln Ser Ser Gly Glu Arg Asn Arg Phe
222 305                      310                      315                      320
225 Ala Asn Arg Ile Lys Ala Leu Asn Arg Leu Lys Ala Lys Leu Leu Val
226                      325                      330                      335
229 Ile Ala Lys Glu Gln Lys Val Ser Asp Val Asn Lys Ile Asp Ser Lys
230                      340                      345                      350
233 Asn Ile Leu Glu Pro Arg Glu Glu Thr Arg Ser Tyr Val Ser Lys Gly
234                      355                      360                      365
237 His Lys Met Val Val Asp Arg Lys Thr Gly Leu Glu Ile Leu Asp Leu
238                      370                      375                      380
241 Lys Ser Val Leu Asp Gly Asn Ile Gly Pro Leu Leu Gly Ala His Ile
242 385                      390                      395                      400
245 Ser Met Arg Arg Ser Ile Asp Ala Ile
246                      405
249 <210> SEQ ID NO: 3
250 <211> LENGTH: 4146
251 <212> TYPE: DNA
252 <213> ORGANISM: Arabidopsis thaliana
254 <220> FEATURE:
255 <221> NAME/KEY: CDS
256 <222> LOCATION: (1)..(4146)
257 <223> OTHER INFORMATION:

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W--> 260 <400> 3
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263 1                      5                      10                      15
265 gag cat ctc tct tcg ctc act aac agt acc aaa cat tct ttc ctc cgg      96
266 Glu His Leu Ser Ser Leu Thr Asn Ser Thr Lys His Ser Phe Leu Arg
267                      20                      25                      30
269 aag aaa cac aga tca acc aaa cca gcc aaa tct ttc ttc aag gtg aaa      144
270 Lys Lys His Arg Ser Thr Lys Pro Ala Lys Ser Phe Phe Lys Val Lys
271                      35                      40                      45
273 tct gct gta tct gga aac ggc ctc ttc aca cag acg aac ccg gag gtc      192
274 Ser Ala Val Ser Gly Asn Gly Leu Phe Thr Gln Thr Asn Pro Glu Val
275                      50                      55                      60
277 cgt cgt ata gtt ccg atc aag aga gac aac gtt ccg acg gtg aaa atc      240
278 Arg Arg Ile Val Pro Ile Lys Arg Asp Asn Val Pro Thr Val Lys Ile
279 65                      70                      75                      80
281 gtc tac gtc gtc ctc gag gct cag tac cag tct tct ctc agt gaa gcc      288
282 Val Tyr Val Val Leu Glu Ala Gln Tyr Gln Ser Ser Leu Ser Glu Ala
283                      85                      90                      95
285 gtg caa tct ctc aac aag act tcg aga ttc gca tcc tac gaa gtg gtt      336
286 Val Gln Ser Leu Asn Lys Thr Ser Arg Phe Ala Ser Tyr Glu Val Val
287                      100                     105                     110
289 gga tac ttg gtc gag gag ctt aga gac aag aac act tac aac aac ttc      384
290 Gly Tyr Leu Val Glu Glu Leu Arg Asp Lys Asn Thr Tyr Asn Asn Phe
291                      115                     120                     125
293 tgc gaa gac ctt aaa gac gcc aac atc ttc att ggt tct ctg atc ttc      432
294 Cys Glu Asp Leu Lys Asp Ala Asn Ile Phe Ile Gly Ser Leu Ile Phe

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Input Set : A:\532622010700seq.txt

Output Set: N:\CRF4\02282005\J524765.raw

295	130	135	140	
297	gag gaa ttg gcg att aaa gtt aag gat gcg gtg gag aag gag aga	480		
298	Val Glu Glu Leu Ala Ile Lys Val Lys Asp Ala Val Glu Lys Glu Arg			
299	145 150 155 160			
301	gac agg atg gac gca gtt ctt gtc ttc cct tca atg cct gag gta atg	528		
302	Asp Arg Met Asp Ala Val Leu Val Phe Pro Ser Met Pro Glu Val Met			
303	165 170 175			
305	aga ctg aac aag ctt gga tct ttt agt atg tct caa ttg ggt cag tca	576		
306	Arg Leu Asn Lys Leu Gly Ser Phe Ser Met Ser Gln Leu Gly Gln Ser			
307	180 185 190			
309	aag tct ccg ttt ttc caa ctc ttc aag agg aag aaa caa ggc tct gct	624		
310	Lys Ser Pro Phe Phe Gln Leu Phe Lys Arg Lys Lys Gln Gly Ser Ala			
311	195 200 205			
313	ggt ttt gcc gat agt atg ttg aag ctt gtt agg act ttg cct aag gtt	672		
314	Gly Phe Ala Asp Ser Met Leu Lys Leu Val Arg Thr Leu Pro Lys Val			
315	210 215 220			
317	ttg aag tac tta cct agt gac aag gct caa gat gct cgt ctc tac atc	720		
318	Leu Lys Tyr Leu Pro Ser Asp Lys Ala Gln Asp Ala Arg Leu Tyr Ile			
319	225 230 235 240			
321	ttg agt tta cag ttt tgg ctt gga ggc tct cct gat aat ctt cag aat	768		
322	Leu Ser Leu Gln Phe Trp Leu Gly Gly Ser Pro Asp Asn Leu Gln Asn			
323	245 250 255			
325	ttt gtt aag atg att tct gga tct tat gtt ccg gct ttg aaa ggt gtc	816		
326	Phe Val Lys Met Ile Ser Gly Ser Tyr Val Pro Ala Leu Lys Gly Val			
327	260 265 270			
329	aaa atc gag tat tcg gat ccg gtt ttg ttc ttg gat act gga att tgg	864		
330	Lys Ile Glu Tyr Ser Asp Pro Val Leu Phe Leu Asp Thr Gly Ile Trp			
331	275 280 285			
333	cat cca ctt gct cca acc atg tac gat gat gtg aag gag tac tgg aac	912		
334	His Pro Leu Ala Pro Thr Met Tyr Asp Asp Val Lys Glu Tyr Trp Asn			
335	290 295 300			
337	tgg tat gac act aga agg gac acc aat gac tca ctc aag agg aaa gat	960		
338	Trp Tyr Asp Thr Arg Arg Asp Thr Asn Asp Ser Leu Lys Arg Lys Asp			
339	305 310 315 320			
341	gca acg gtt gtc ggt tta gtc ttg cag agg agt cac att gtg act ggt	1008		
342	Ala Thr Val Val Gly Leu Val Leu Gln Arg Ser His Ile Val Thr Gly			
343	325 330 335			
345	gat gat agt cac tat gtg gct gtt atc atg gag ctt gag gct aga ggt	1056		
346	Asp Asp Ser His Tyr Val Ala Val Ile Met Glu Leu Glu Ala Arg Gly			
347	340 345 350			
349	gct aag gtc gtt cct ata ttc gca gga ggg ttg gat ttc tct ggt cca	1104		
350	Ala Lys Val Val Pro Ile Phe Ala Gly Gly Leu Asp Phe Ser Gly Pro			
351	355 360 365			
353	gta gag aaa tat ttc gta gac ccg gtg tcg aaa cag ccc atc gta aac	1152		
354	Val Glu Lys Tyr Phe Val Asp Pro Val Ser Lys Gln Pro Ile Val Asn			
355	370 375 380			
357	tct gct gtc tcc ttg act ggt ttt gct ctt gtt ggt gga cct gca agg	1200		
358	Ser Ala Val Ser Leu Thr Gly Phe Ala Leu Val Gly Gly Pro Ala Arg			
359	385 390 395 400			

## VERIFICATION SUMMARY

DATE: 02/28/2005

PATENT APPLICATION: US/10/524,765

TIME: 10:16:58

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Output Set: N:\CRF4\02282005\J524765.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:32 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:29  
L:260 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:257  
L:984 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:981  
L:1332 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:1329  
L:1602 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:1599  
L:1760 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:1757  
L:2028 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:13,Line#:2025  
L:2192 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:15,Line#:2189  
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